

IN THE SEQUENCE LISTING

Kindly enter the attached Sequence Listing in lieu of the original translation.

10/534002

SEQUENCE LISTING

JC20 Rec'd PCT/PTO 05 MAY 2005

<110> NARIMATSU, Hisashi
SATO, Takashi
GOTOH, Masanori

<120> METHOD OF DETECTING BONE PAGET'S DISEASE

<130> 159-88 / YCT-882

<140> US

<141> 2005-05-05

<150> PCT/JP2003/014211

<151> 2003-11-07

<150> JP2002-323438

<151> 2002-11-07

<160> 70

<170> MS Word

<210> 1

<211> 2649

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2649)

<400> 1

atg gct gtg cgc tct cgc cgc ccg tgg atg agc gtg gca tta ggg ctg	48
Met Ala Val Arg Ser Arg Arg Pro Trp Met Ser Val Ala Leu Gly Leu	
1 5 10 15	

gtg ctg ggc ttc acc gcc gcg tcc tgg ctc atc gcc ccc agg gtg gcg	96
Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala	
20 25 30	

gag ctg agc gag agg aag aga cgt ggc tcc agc ctc tgc tcc tac tac	144
Glu Leu Ser Glu Arg Lys Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr	
35 40 45	

ggt cgc tct gct gct ggc ccc cgc gcc ggc gct cag cag ccg ctc ccc	192
Gly Arg Ser Ala Ala Gly Pro Arg Ala Gly Ala Gln Gln Pro Leu Pro	
50 55 60	

cag ccc cag tcc cga cca ccg cag gag cag tcc ccg ccc ccc gcg cgc	240
Gln Pro Gln Ser Arg Pro Arg Gln Glu Gln Ser Pro Pro Pro Ala Arg	
65 70 75 80	

cag gat ctc cag ggg cca ccg ctg ccc gag gca gca ccc ggg atc acc	288
Gln Asp Leu Gln Gly Pro Pro Leu Pro Glu Ala Ala Pro Gly Ile Thr	
85 90 95	

agt ttt cga agc agc ccc tgg cag cag cca cct ccg ctg cag cag cgg	336
Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Pro Pro Leu Gln Gln Arg	
100 105 110	
cgg cga gga cgc gag cct gag ggc gcg acg ggg ctt ccc ggt gct cca	384
Arg Arg Gly Arg Glu Pro Glu Gly Ala Thr Gly Leu Pro Gly Ala Pro	
115 120 125	
gcg gcc gag ggg gag ccc gag gag gag gac ggg ggc gcg gct ggg cag	432
Ala Ala Glu Gly Glu Pro Glu Glu Glu Asp Gly Gly Ala Ala Gly Gln	
130 135 140	
cgg aga gac ggc cgg ccg ggg agt agc cac aac ggc agc ggg gac ggg	480
Arg Arg Asp Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly	
145 150 155 160	
ggc gct gcc gcc ccg agc gcc cga ccc ccg gac ttc ctg tac gtg ggg	528
Gly Ala Ala Ala Pro Ser Ala Arg Pro Arg Asp Phe Leu Tyr Val Gly	
165 170 175	
gtg atg acc gcg cag aag tac ctg ggc agc cgc gcg ctg gcc gcg cag	576
Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln	
180 185 190	
cgg acc tgg gcg cgt ttc atc ccg ggc cgc gtg gag ttc ttt tcc agc	624
Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser	
195 200 205	
cag cag ccc ccc aac gcc ggc cag ccc ccg cca ccc ctg cct gtc atc	672
Gln Gln Pro Pro Asn Ala Gly Gln Pro Pro Pro Pro Leu Pro Val Ile	
210 215 220	
gcg cta ccg ggt gtg gac gac tcc tat cct ccc cag aaa aag tcc ttc	720
Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe	
225 230 235 240	
atg atg atc aag tac atg cac gac cac tac ctg gac aag tat gag tgg	768
Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu Trp	
245 250 255	
ttc atg cgc gcc gac gac gat gtc tac atc aaa ggt gat aaa tta gaa	816
Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Lys Leu Glu	
260 265 270	
gag ttt ctt aga tcg cta aac agc agt aag cct ctc tac ctg gga cag	864
Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu Gly Gln	
275 280 285	
act ggc ctg ggg aat att gaa gag ctt gga aag ctg gga ctg gag cct	912
Thr Gly Leu Gly Asn Ile Glu Glu Leu Gly Lys Leu Gly Leu Glu Pro	
290 295 300	
ggg gaa aac ttc tgt atg gga gga cct ggc atg atc ttt agc cga gaa	960
Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser Arg Glu	
305 310 315 320	

gtt ctc agg agg atg gtg cca cat att ggt gaa tgc ctt aga gaa atg Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg Glu Met 325 330 335	1008
tac acg act cat gag gat gtg gaa gta gga aga tgc gtt cgc cgt ttt Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg Arg Phe 340 345 350	1056
ggg ggg act cag tgt gtc tgg tct tac gag atg caa caa ctg ttc cat Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu Phe His 355 360 365	1104
gaa aat tat gaa cac aat cgg aag ggt tac atc caa gac ctt cac aat Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu His Asn 370 375 380	1152
agc aaa atc cat gca gcc ata aca ctt cat ccc aac aaa agg cct gca Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg Pro Ala 385 390 395 400	1200
tac caa tac agg ctg cat aat tac atg ctc agc cgc aaa att tct gaa Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile Ser Glu 405 410 415	1248
ctt cgc tac cgc acc atc cag ctc cac agg gaa agt gcc ctg atg agc Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu Met Ser 420 425 430	1296
aag ctc agt aac aca gaa gtg agc aaa gag gac cag cag ctg gga gtg Lys Leu Ser Asn Thr Glu Val Ser Lys Glu Asp Gln Gln Leu Gly Val 435 440 445	1344
ata cct tct ttc aac cac ttc cag cct cgg gag aga aat gaa gtg ata Ile Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu Val Ile 450 455 460	1392
gaa tgg gag ttc ctg aca ggg aag ctt cta tac tca gca gct gag aac Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala Glu Asn 465 470 475 480	1440
cag ccc cct cga cag agc ctc agt agc att tta aga aca gca ctg gat Gln Pro Pro Arg Gln Ser Leu Ser Ser Ile Leu Arg Thr Ala Leu Asp 485 490 495	1488
gat acc gtc cta cag gtg atg gag atg atc aat gag aat gcc aag agc Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala Lys Ser 500 505 510	1536
aga gga cgg ctc att gac ttc aag gaa att cag tat ggc tac cgc aga Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr Arg Arg 515 520 525	1584
gtt aac ccc atg cac ggg gtg gag tac att ttg gat tta ctc ctt tta Val Asn Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu Leu Leu 530 535 540	1632

tac aaa aga cac aag gga agg aaa ctg act gtg cca gtg aga cgt cat	1680
Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg Arg His	
545 550 555 560	
gcc tat ctt cag cag ttg ttc agc aag cct ttc ttc aga gag acc gaa	1728
Ala Tyr Leu Gln Gln Leu Phe Ser Lys Pro Phe Phe Arg Glu Thr Glu	
565 570 575	
gag cta gat gtc aac agt ctt gtg gag agt att aac agt gaa act cag	1776
Glu Leu Asp Val Asn Ser Leu Val Glu Ser Ile Asn Ser Glu Thr Gln	
580 585 590	
tca ttc tcc ttt ata tct aat tct tta aag ata tta tct tct ttt caa	1824
Ser Phe Ser Phe Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser Phe Gln	
595 600 605	
ggt gcc aaa gaa atg gga ggg cac aat gaa aag aaa gta cac att ctc	1872
Gly Ala Lys Glu Met Gly Gly His Asn Glu Lys Lys Val His Ile Leu	
610 615 620	
gtt cct ctc atc gga agg tat gac att ttc ttg aga ttc atg gag aac	1920
Val Pro Leu Ile Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met Glu Asn	
625 630 635 640	
ttt gaa aac atg tgt ctt atc cca aag cag aat gta aag ttg gtc att	1968
Phe Glu Asn Met Cys Leu Ile Pro Lys Gln Asn Val Lys Leu Val Ile	
645 650 655	
atc ctt ttc agt agg gat tct ggc caa gac tcc agc aag cat att gag	2016
Ile Leu Phe Ser Arg Asp Ser Gly Gln Asp Ser Ser Lys His Ile Glu	
660 665 670	
ctg ata aaa ggg tac cag aac aag tac ccc aaa gca gaa atg acc ctg	2064
Leu Ile Lys Gly Tyr Gln Asn Lys Tyr Pro Lys Ala Glu Met Thr Leu	
675 680 685	
atc cca atg aag gga gag ttt tcc aga ggt ctt ggt ctt gaa atg gct	2112
Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu Met Ala	
690 695 700	
tct gcc cag ttt gac aat gac act ttg ctg cta ttt tgt gat gtt gac	2160
Ser Ala Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp Val Asp	
705 710 715 720	
ttg atc ttc aga gaa gat ttt ctc caa cga tgt aga gac aat aca att	2208
Leu Ile Phe Arg Glu Asp Phe Leu Gln Arg Cys Arg Asp Asn Thr Ile	
725 730 735	
cag gga caa cag gtg tac tat ccc atc atc ttt agc cag tat gac cca	2256
Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr Asp Pro	
740 745 750	
aag gta aca aac ggg gga aat cct ccc act gat ggt tac ttc ata ttc	2304
Lys Val Thr Asn Gly Gly Asn Pro Pro Thr Asp Gly Tyr Phe Ile Phe	
755 760 765	

tca aaa aag act gga ttt tgg aga gac tat gga tat ggc atc acc tgt	2352
Ser Lys Lys Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile Thr Cys	
770 775 780	
att tac aaa agt gat ctt cta ggt gca ggt gga ttt gat acc tca ata	2400
Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr Ser Ile	
785 790 795 800	
caa ggc tgg gga cta gaa gat gta gat ctc tac aat aaa gtc att cta	2448
Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val Ile Leu	
805 810 815	
tct ggc tta agg cca ttc aga agc caa gaa gta gga gtg gtg cat att	2496
Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val His Ile	
820 825 830	
ttc cat cca gtt cat tgt gat cct aac ttg gac cct aag cag tat aag	2544
Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys	
835 840 845	
atg tgc tta gga tcc aag gca agt act ttc gcc tca acc atg caa ctg	2592
Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met Gln Leu	
850 855 860	
gct gaa ctc tgg ctt gaa aaa cat tta ggt gtc agg tac aat cga act	2640
Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Tyr Asn Arg Thr	
865 870 875 880	
ctc tcc tga	2649
Leu Ser	

<210> 2
 <211> 882
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Val Arg Ser Arg Arg Pro Trp Met Ser Val Ala Leu Gly Leu
 1 5 10 15
 Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala
 20 25 30
 Glu Leu Ser Glu Arg Lys Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr
 35 40 45
 Gly Arg Ser Ala Ala Gly Pro Arg Ala Gly Ala Gln Gln Pro Leu Pro
 50 55 60
 Gln Pro Gln Ser Arg Pro Arg Gln Glu Gln Ser Pro Pro Pro Ala Arg
 65 70 75 80
 Gln Asp Leu Gln Gly Pro Pro Leu Pro Glu Ala Ala Pro Gly Ile Thr
 85 90 95

Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Pro Pro Leu Gln Gln Arg
 100 105 110
 Arg Arg Gly Arg Glu Pro Glu Gly Ala Thr Gly Leu Pro Gly Ala Pro
 115 120 125
 Ala Ala Glu Gly Glu Pro Glu Glu Glu Asp Gly Gly Ala Ala Gly Gln
 130 135 140
 Arg Arg Asp Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly
 145 150 155 160
 Gly Ala Ala Ala Pro Ser Ala Arg Pro Arg Asp Phe Leu Tyr Val Gly
 165 170 175
 Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln
 180 185 190
 Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser
 195 200 205
 Gln Gln Pro Pro Asn Ala Gly Gln Pro Pro Pro Pro Leu Pro Val Ile
 210 215 220
 Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
 225 230 235 240
 Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu Trp
 245 250 255
 Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Lys Leu Glu
 260 265 270
 Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu Gly Gln
 275 280 285
 Thr Gly Leu Gly Asn Ile Glu Glu Leu Gly Lys Leu Gly Leu Glu Pro
 290 295 300
 Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser Arg Glu
 305 310 315 320
 Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg Glu Met
 325 330 335
 Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg Arg Phe
 340 345 350
 Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu Phe His
 355 360 365
 Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu His Asn
 370 375 380
 Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg Pro Ala
 385 390 395 400

Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile Ser Glu
 405 410 415
 Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu Met Ser
 420 425 430
 Lys Leu Ser Asn Thr Glu Val Ser Lys Glu Asp Gln Gln Leu Gly Val
 435 440 445
 Ile Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu Val Ile
 450 455 460
 Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala Glu Asn
 465 470 475 480
 Gln Pro Pro Arg Gln Ser Leu Ser Ser Ile Leu Arg Thr Ala Leu Asp
 485 490 495
 Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala Lys Ser
 500 505 510
 Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr Arg Arg
 515 520 525
 Val Asn Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu Leu Leu
 530 535 540
 Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg Arg His
 545 550 555 560
 Ala Tyr Leu Gln Gln Leu Phe Ser Lys Pro Phe Phe Arg Glu Thr Glu
 565 570 575
 Glu Leu Asp Val Asn Ser Leu Val Glu Ser Ile Asn Ser Glu Thr Gln
 580 585 590
 Ser Phe Ser Phe Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser Phe Gln
 595 600 605
 Gly Ala Lys Glu Met Gly Gly His Asn Glu Lys Lys Val His Ile Leu
 610 615 620
 Val Pro Leu Ile Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met Glu Asn
 625 630 635 640
 Phe Glu Asn Met Cys Leu Ile Pro Lys Gln Asn Val Lys Leu Val Ile
 645 650 655
 Ile Leu Phe Ser Arg Asp Ser Gly Gln Asp Ser Ser Lys His Ile Glu
 660 665 670
 Leu Ile Lys Gly Tyr Gln Asn Lys Tyr Pro Lys Ala Glu Met Thr Leu
 675 680 685
 Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu Met Ala
 690 695 700

Ser Ala Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp Val Asp
 705 710 715 720
 Leu Ile Phe Arg Glu Asp Phe Leu Gln Arg Cys Arg Asp Asn Thr Ile
 725 730 735
 Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr Asp Pro
 740 745 750
 Lys Val Thr Asn Gly Gly Asn Pro Pro Thr Asp Gly Tyr Phe Ile Phe
 755 760 765
 Ser Lys Lys Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile Thr Cys
 770 775 780
 Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr Ser Ile
 785 790 795 800
 Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val Ile Leu
 805 810 815
 Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val His Ile
 820 825 830
 Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys
 835 840 845
 Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met Gln Leu
 850 855 860
 Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Tyr Asn Arg Thr
 865 870 875 880
 Leu Ser

<210> 3
 <211> 2328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2328)

<400> 3
 atg cgg gca tcg ctg ctg ctg tcg gtg ctg cgg ccc gca ggg ccc gtg
 Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro Val
 1 5 10 15

48

gcc gtg ggc atc tcc ctg ggc ttc acc ctg agc ctg ctc agc gtc acc
 Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr
 20 25 30

96

tgg gtg gag gag ccg tgc ggc cca ggc ccg ccc caa cct gga gac tct	144
Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro Gly Asp Ser	
35 40 45	
gag ctg ccg ccg cgc ggc aac acc aac gcg gcg cgc cgg ccc aac tcg	192
Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser	
50 55 60	
gtg cag ccc gga gcg gag cgc gag aag ccc ggg gcc ggc gaa ggc gcc	240
Val Gln Pro Gly Ala Glu Arg Glu Lys Pro Gly Ala Gly Glu Gly Ala	
65 70 75 80	
ggg gag aat tgg gag ccg cgc gtc ttg ccc tac cac cct gca cag ccc	288
Gly Glu Asn Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro	
85 90 95	
ggc cag gcc gcc aaa aag gcc gtc agg acc cgc tac atc agc acg gag	336
Gly Gln Ala Ala Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu	
100 105 110	
ctg ggc atc agg cag agg ctg ctg gtg gcg gtg ctg acc tct cag acc	384
Leu Gly Ile Arg Gln Arg Leu Leu Val Ala Val Leu Thr Ser Gln Thr	
115 120 125	
acg ctg ccc acg ctg ggc gtg gcc gtg aac cgc acg ctg ggg cac cgg	432
Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg	
130 135 140	
ctg gag cgt gtg gtg ttc ctg acg ggc gca cgg ggc cgc cgg gcc cca	480
Leu Glu Arg Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Ala Pro	
145 150 155 160	
cct ggc atg gca gtg gtg acg ctg ggc gag gag cga ccc att gga cac	528
Pro Gly Met Ala Val Val Thr Leu Gly Glu Glu Arg Pro Ile Gly His	
165 170 175	
ctg cac ctg gcg ctg cgc cac ctg ctg gag cag cac ggc gac gac ttt	576
Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe	
180 185 190	
gac tgg ttc ttc ctg gtg cct gac acc acc tac acc gag gcg cac ggc	624
Asp Trp Phe Phe Leu Val Pro Asp Thr Thr Tyr Thr Glu Ala His Gly	
195 200 205	
ctg gca cgc cta act ggc cac ctc agc ctg gcc tcc gcc gcc cac ctg	672
Leu Ala Arg Leu Thr Gly His Leu Ser Leu Ala Ser Ala Ala His Leu	
210 215 220	
tac ctg ggc cgg ccc cag gac ttc atc ggc gga gag ccc acc ccc ggc	720
Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Glu Pro Thr Pro Gly	
225 230 235 240	
cgc tac tgc cac gga ggc ttt ggg gtg ctg ctg tcg cgc atg ctg ctg	768
Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Met Leu Leu	
245 250 255	

caa caa ctg cgc ccc cac ctg gaa ggc tgc cgc aac gac atc gtc agt	816
Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile Val Ser	
260 265 270	
gcg cgc cct gac gag tgg ctg ggt cgc tgc att ctc gat gcc acc ggg	864
Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly	
275 280 285	
gtg ggc tgc act ggt gac cac gag ggg gtg cac tat agc cat ctg gag	912
Val Gly Cys Thr Gly Asp His Glu Gly Val His Tyr Ser His Leu Glu	
290 295 300	
ctg agc cct ggg gag cca gtg cag gag ggg gac cct cat ttc cga agt	960
Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro His Phe Arg Ser	
305 310 315 320	
gcc ctg aca gcc cac cct gtg cgt gac cct gtg cac atg tac cag ctg	1008
Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu	
325 330 335	
cac aaa gct ttc gcc cga gct gaa ctg gaa cgc acg tac cag gag atc	1056
His Lys Ala Phe Ala Arg Ala Glu Leu Glu Arg Thr Tyr Gln Glu Ile	
340 345 350	
cag gag tta cag tgg gag atc cag aat acc agc cat ctg gcc gtt gat	1104
Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser His Leu Ala Val Asp	
355 360 365	
ggg gac cgg gca gct gct tgg ccc gtg ggt att cca gca cca tcc cgc	1152
Gly Asp Arg Ala Ala Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg	
370 375 380	
ccg gcc tcc cgc ttt gag gtg ctg cgc tgg gac tac ttc acg gag cag	1200
Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln	
385 390 395 400	
cac gct ttc tcc tgc gcc gat ggc tca ccc cgc tgc cca ctg cgt ggg	1248
His Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly	
405 410 415	
gct gac cgg gct gat gtg gcc gat gtt ctg ggg aca gct cta gag gag	1296
Ala Asp Arg Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu	
420 425 430	
ctg aac cgc cgc tac cac ccg gcc ttg cgg ctc cag aag cag cag ctg	1344
Leu Asn Arg Arg Tyr His Pro Ala Leu Arg Leu Gln Lys Gln Gln Leu	
435 440 445	
gtg aat ggc tac cga cgc ttt gat ccg gcc cgg ggt atg gaa tac acg	1392
Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr	
450 455 460	
ctg gac ttg cag ctg gag gca ctg acc ccc cag gga ggc cgc cgg ccc	1440
Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro	
465 470 475 480	

ctc act cgc cga gtg cag ctg ctc cgg ccg ctg agc cgc gtg gag atc	1488
Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile	
485 490 495	
ttg cct gtg ccc tat gtc act gag gcc tca cgt ctc act gtg ctg ctg	1536
Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu	
500 505 510	
cct cta gct gcg gct gag cgt gac ctg gcc cct ggc ttc ttg gag gcc	1584
Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe Leu Glu Ala	
515 520 525	
ttt gcc act gca gca ctg gag cct ggt gat gct gcg gca gcc ctg acc	1632
Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Leu Thr	
530 535 540	
ctg ctg cta ctg tat gag ccg cgc cag gcc cag cgc gtg gcc cat gca	1680
Leu Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Val Ala His Ala	
545 550 555 560	
gat gtc ttc gca cct gtc aag gcc cac gtg gca gag ctg gag cgg cgt	1728
Asp Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg	
565 570 575	
ttc ccc ggt gcc cgg gtg cca tgg ctc agt gtg cag aca gcc gca ccc	1776
Phe Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro	
580 585 590	
tca cca ctg cgc ctc atg gat cta ctc tcc aag aag cac ccg ctg gac	1824
Ser Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp	
595 600 605	
aca ctg ttc ctg ctg gcc ggg cca gac acg gtg ctc acg cct gac ttc	1872
Thr Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe	
610 615 620	
ctg aac cgc tgc cgc atg cat gcc atc tcc ggc tgg cag gcc ttc ttt	1920
Leu Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe	
625 630 635 640	
ccc atg cat ttc caa gcc ttc cac cca gct gtg gcc cca cca caa ggg	1968
Pro Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly	
645 650 655	
cct ggg ccc cca gag ctg ggc cgt gac act ggc cgc ttt gat cgc cag	2016
Pro Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly Arg Phe Asp Arg Gln	
660 665 670	
gca gcc agc gag gcc tgc ttc tac aac tcc gac tac gtg gca gcc cgt	2064
Ala Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg	
675 680 685	
ggg cgc ctg gcg gca gcc tca gaa caa gaa gag gag ctg ctg gag agc	2112
Gly Arg Leu Ala Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser	
690 695 700	

ctg gat gtg tac gag ctg ttc ctc cac ttc tcc agt ctg cat gtg ctg	2160
Leu Asp Val Tyr Glu Leu Phe Leu His Phe Ser Ser Leu His Val Leu	
705 710 715 720	
cgg gcg gtg gag ccg gcg ctg ctg cag cgc tac cgg gcc cag acg tgc	2208
Arg Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Thr Cys	
725 730 735	
agc gcg agg ctc agt gag gac ctg tac cac cgc tgc ctc cag agc gtg	2256
Ser Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Leu Gln Ser Val	
740 745 750	
ctt gag ggc ctc ggc tcc cga acc cag ctg gcc atg cta ctc ttt gaa	2304
Leu Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu	
755 760 765	
cag gag cag ggc aac agc acc tga	2328
Gln Glu Gln Gly Asn Ser Thr	
770 775	

<210> 4
 <211> 775
 <212> PRT
 <213> Homo sapiens

<400> 4	
Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro Val	
1 5 10 15	
Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr	
20 25 30	
Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro Gly Asp Ser	
35 40 45	
Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser	
50 55 60	
Val Gln Pro Gly Ala Glu Arg Glu Lys Pro Gly Ala Gly Glu Gly Ala	
65 70 75 80	
Gly Glu Asn Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro	
85 90 95	
Gly Gln Ala Ala Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu	
100 105 110	
Leu Gly Ile Arg Gln Arg Leu Leu Val Ala Val Leu Thr Ser Gln Thr	
115 120 125	
Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg	
130 135 140	
Leu Glu Arg Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Ala Pro	
145 150 155 160	

Pro Gly Met Ala Val Val Thr Leu Gly Glu Glu Arg Pro Ile Gly His
 165 170 175
 Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe
 180 185 190
 Asp Trp Phe Phe Leu Val Pro Asp Thr Thr Tyr Thr Glu Ala His Gly
 195 200 205
 Leu Ala Arg Leu Thr Gly His Leu Ser Leu Ala Ser Ala Ala His Leu
 210 215 220
 Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Glu Pro Thr Pro Gly
 225 230 235 240
 Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Met Leu Leu
 245 250 255
 Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile Val Ser
 260 265 270
 Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly
 275 280 285
 Val Gly Cys Thr Gly Asp His Glu Gly Val His Tyr Ser His Leu Glu
 290 295 300
 Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro His Phe Arg Ser
 305 310 315 320
 Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu
 325 330 335
 His Lys Ala Phe Ala Arg Ala Glu Leu Glu Arg Thr Tyr Gln Glu Ile
 340 345 350
 Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser His Leu Ala Val Asp
 355 360 365
 Gly Asp Arg Ala Ala Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg
 370 375 380
 Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln
 385 390 395 400
 His Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly
 405 410 415
 Ala Asp Arg Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu
 420 425 430
 Leu Asn Arg Arg Tyr His Pro Ala Leu Arg Leu Gln Lys Gln Gln Leu
 435 440 445
 Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr
 450 455 460

Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro
 465 470 475 480
 Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile
 485 490 495
 Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu
 500 505 510
 Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe Leu Glu Ala
 515 520 525
 Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Ala Leu Thr
 530 535 540
 Leu Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Val Ala His Ala
 545 550 555 560
 Asp Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg
 565 570 575
 Phe Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro
 580 585 590
 Ser Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp
 595 600 605
 Thr Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe
 610 615 620
 Leu Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe
 625 630 635 640
 Pro Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly
 645 650 655
 Pro Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly Arg Phe Asp Arg Gln
 660 665 670
 Ala Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg
 675 680 685
 Gly Arg Leu Ala Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser
 690 695 700
 Leu Asp Val Tyr Glu Leu Phe Leu His Phe Ser Ser Leu His Val Leu
 705 710 715 720
 Arg Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Thr Cys
 725 730 735
 Ser Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Leu Gln Ser Val
 740 745 750
 Leu Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu
 755 760 765

Gln Glu Gln Gly Asn Ser Thr
770 775

<210> 5
<211> 1669
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (41)..(1024)

<400> 5
ctgCGagcgc ctgccccatg cgccgcgcgc tctccgcacg atg ttc ccc tcg cgg 55
Met Phe Pro Ser Arg
1 5

agg aaa gcg gcg cag ctg ccc tgg gag gac ggc agg tcc ggg ttg ctc 103
Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly Arg Ser Gly Leu Leu
10 15 20

tcc ggc ggc ctc cct cgg aag tgt tcc gtc ttc cac ctg ttc gtg gcc 151
Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe His Leu Phe Val Ala
25 30 35

tgc ctc tcg ctg ggc ttc ttc tcc cta ctc tgg ctg cag ctc agc tgc 199
Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp Leu Gln Leu Ser Cys
40 45 50

tct ggg gac gtg gcc cgg gca gtc agg gga caa ggg cag gag acc tcg 247
Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln Gly Gln Glu Thr Ser
55 60 65

ggc cct ccc cgc gcc tgc ccc cca gag ccg ccc cct gag cac tgg gaa 295
Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro Pro Glu His Trp Glu
70 75 80 85

gaa gac gca tcc tgg ggc ccc cac cgc ctg gca gtg ctg gtg ccc ttc 343
Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala Val Leu Val Pro Phe
90 95 100

cgc gaa cgc ttc gag gag ctc ctg gtc ttc gtg ccc cac atg cgc cgc 391
Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg
105 110 115

ttc ctg agc agg aag aag atc cgg cac cac atc tac gtg ctc aac cag 439
Phe Leu Ser Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln
120 125 130

gtg gac cac ttc agg ttc aac cgg gca gcg ctc atc aac gtg ggc ttc 487
Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe
135 140 145

ctg gag agc agc aac agc acg gac tac att gcc atg cac gac gtt gac	535
Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp	
150 155 160 165	
ctg ctc cct ctc aac gag gag ctg gac tat ggc ttt cct gag gct ggg	583
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala Gly	
170 175 180	
ccc ttc cac gtg gcc tcc ccg gag ctc cac cct ctc tac cac tac aag	631
Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His Tyr Lys	
185 190 195	
acc tat gtc ggc ggc atc ctg ctg ctc tcc aag cag cac tac cgg ctg	679
Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His Tyr Arg Leu	
200 205 210	
tgc aat ggg atg tcc aac cgc ttc tgg ggc tgg ggc cgc gag gac gac	727
Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly Arg Glu Asp Asp	
215 220 225	
gag ttc tac cgg cgc att aag gga gct ggc ctc cag ctt ttc cgc ccc	775
Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu Gln Leu Phe Arg Pro	
230 235 240 245	
tcg gga atc aca act ggg tac aag aca ttt cgc cac ctg cac gac cca	823
Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg His Leu His Asp Pro	
250 255 260	
gcc tgg cgg aag agg gac cag aag cgc atc gca gct caa aaa cag gag	871
Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala Ala Gln Lys Gln Glu	
265 270 275	
cag ttc aag gtg gac agg gag gga ggc ctg aac act gtg aag tac cat	919
Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn Thr Val Lys Tyr His	
280 285 290	
gtg gct tcc cgc act gcc ctg tct gtg ggc ggg gcc ccc tgc act gtc	967
Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly Ala Pro Cys Thr Val	
295 300 305	
ctc aac atc atg ttg gac tgt gac aag acc gcc aca ccc tgg tgc aca	1015
Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr	
310 315 320 325	
ttc agc tga gctggatgga cagtgaggaa gcctgtacct acaggccata	1064
Phe Ser	
ttgctcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg atgtggagtg	1124
gccaggacca agacagcaag ctacgcaatt gcagccaccc ggccgccaag gcaggcttgg	1184
gctgggcccag gacacgtggg gtgcctggga cgctgcttgc catgcacagt gatcagagag	1244
aggctgggggt gtgtcctgtc cgggaccccc cctgccttcc tgctcacctt actctgacct	1304
ccttcacgtg cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac	1364

cccactttt gttccttct gctgggctgc ctcgtgcaga gacacagtgt agggggccatg 1424
 cagctggcgt aggtggcagt tgggcctggt gaggggttagg acttcagaaa ccagagcaca 1484
 agccccacag aggggggaaca gccagcaccg ctctagctgg ttgttgccat gccggaatgt 1544
 gggcctagtg ttgccagatc ttctgatttt tcgaaagaaa ctagaatgct ggattcttaa 1604
 gtgatatctt ctgatttttt aaatgatagc acctaaatga aactttcaaa aagtaaaaaa 1664
 aaaaa 1669

<210> 6.
 <211> 327
 <212> PRT
 <213> Homo sapiens

<400> 6

Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp	Gly	
1				5					10					15		
Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser	Val	Phe	
			20					25					30			
His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser	Leu	Leu	Trp	
			35					40				45				
Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala	Val	Arg	Gly	Gln	
	50					55					60					
Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys	Pro	Pro	Glu	Pro	Pro	
65					70					75					80	
Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp	Gly	Pro	His	Arg	Leu	Ala	
				85					90					95		
Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe	Glu	Glu	Leu	Leu	Val	Phe	Val	
			100					105					110			
Pro	His	Met	Arg	Arg	Phe	Leu	Ser	Arg	Lys	Lys	Ile	Arg	His	His	Ile	
		115					120					125				
Tyr	Val	Leu	Asn	Gln	Val	Asp	His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	
	130					135					140					
Ile	Asn	Val	Gly	Phe	Leu	Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	
145					150					155					160	
Met	His	Asp	Val	Asp	Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	
				165				170						175		
Phe	Pro	Glu	Ala	Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	
			180					185					190			

Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
 195 200 205
 Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
 210 215 220
 Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
 225 230 235 240
 Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
 245 250 255
 His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
 260 265 270
 Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
 275 280 285
 Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
 290 295 300
 Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
 305 310 315 320
 Thr Pro Trp Cys Thr Phe Ser
 325

<210> 7
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 5' primer for PCR (K3)

<400> 7
 cccaagcttg ccgaggggga gcccga

26

<210> 8
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 3' primer for PCR (K3)

<400> 8
 gctctagact gtcaggagag agttcgatt

29

<210> 9
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 5' primer for PCR (K3)

 <400> 9
 atggctgtgc gctctcgccg cccgt 25

 <210> 10
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR (K3)

 <400> 10
 cgtccccgct gccgttggtg ctact 25

 <210> 11
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 5' primer for PCR (K3)

 <400> 11
 agtagccaca acggcagcgg ggacg 25

 <210> 12
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR (K3)

 <400> 12
 tcaggagaga gttcgattgt acct 24

 <210> 13
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 5' primer for PCR (K11)

 <400> 13
 ggaattccgg ccaggccgcc aaaaaggc 28

 <210> 14
 <211> 30

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR (K11)

 <400> 14
 cgggatcctc aggtgctgtt gccctgctcc 30

 <210> 15
 <211> 16
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: synthesised substance for
 assay

 <400> 15

 Val Leu Pro Gln Glu Glu Glu Gly Ser Gly Gly Gly Gln Leu Val Thr
 1 5 10 15

 <210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 5' primer for PCR and
 sequencing (K3 exon 1)

 <400> 16
 cgacagccca gcgagcgtcc 20

 <210> 17
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR and
 sequencing (K3 exon 1)

 <400> 17
 ggagactggc aggctggaaa gc 22

 <210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 1)

<400> 18
aggggggagcc cgaggaggag 20

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 1)

<400> 19
ctcctcctcg ggctccccct 20

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and
sequencing (K3 exon 2)

<400> 20
gagacatagt aattggtgcc tttcttt 27

<210> 21
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and
sequencing (K3 exon 2)

<400> 21
gtgaacattt tcatcacagc tccat 25

<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and
sequencing (K3 exon 3)

<400> 22
tagatgcttt agtttatcgc tggttt 26

<210> 23
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR and
 sequencing (K3 exon 3)

 <400> 23
 ttaaaaaagg caaaatgtgt tgcctg 26

 <210> 24
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer for sequencing
 (K3 exon 3)

 <400> 24
 tctataactca gcagctgaga acca 24

 <210> 25
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer for sequencing
 (K3 exon 3)

 <400> 25
 tggttctcag ctgctgagta taga 24

 <210> 26
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer for sequencing
 (K3 exon 3)

 <400> 26
 gaaatgggag ggcacaatga aaag 24

 <210> 27
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 3)

<400> 27
cttttcattg tgccctccca tttc 24

<210> 28
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 3)

<400> 28
tagccagtat gacccaaagg taac 24

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 3)

<400> 29
gttacctttg ggtcatactg gcta 24

<210> 30
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 3)

<400> 30
aggccattca gaagccaaga agtaggagtg g 31

<210> 31
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 3)

<400> 31
 ccactcctac ttcttggtt ctgaatggcc t 31

<210> 32
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 5' primer for PCR and
 sequencing (K11 exon 1)

<400> 32
 tcggagactc ctctggctgc t 21

<210> 33
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Descriprion of Artificial Sequence: 3' primer for PCR and
 sequencing (K11 exon 1)

<400> 33
 tagagcgggc gcagccgatc a 21

<210> 34
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 5' primer for PCR and
 sequencing (K11 exon 2)

<400> 34
 tttgataagc ttgtgccatc tcctc 25

<210> 35
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 3' primer for PCR and
 sequencing (K11 exon 2)

<400> 35
 aggtatcagt gggatagctt atcat 25

<210> 36
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 5' primer for PCR and
 sequencing (K11 exon 3)

 <400> 36
 agctcatcac agatcccttc ctt 24

 <210> 37
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR and
 sequencing (K11 exon 1)

 <400> 37
 actctgccac cccagacct ag 22

 <210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 5' primer for PCR and
 sequencing (K11 exon 4)

 <400> 38
 ttgctgatgg cctgtttctc tgat 24

 <210> 39
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR and
 sequencing (K11 exon 4)

 <400> 39
 gtgtggccat gccacggccc a 21

 <210> 40
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer for sequencing
 (K11 exon 4)

<400> 40
 tatgtcactg aggcctcacg tct 23

<210> 41
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer for sequencing
 (K11 exon 4)

<400> 41
 agacgtgagg cctcagtgac ata 23

<210> 42
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer for sequencing
 (K11 exon 4)

<400> 42
 atgcatttcc aagccttcca ccca 24

<210> 43
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer for sequencing
 (K11 exon 4)

<400> 43
 tgggtggaag gcttggaat gcat 24

<210> 44
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 5' primer for PCR and
 sequencing (beta4Gal-T7 exon 1)

<400> 44

tgcgagcgcc tgcccatgc 20

<210> 45
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and
sequencing (beta4Gal-T7 exon 1)

<400> 45
gatggcctcg ggttcccaga tt 22

<210> 46
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and
sequencing (beta4Gal-T7 exon 2)

<400> 46
tcctgaccct gtcccgcgct t 21

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and
sequencing (beta4Gal-T7 exon 2)

<400> 47
aggggtgccg aggggagagg 20

<210> 48
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and
sequencing (beta4Gal-T7 exon 3)

<400> 48
ctgccagcc ttgccaccc t 21

<210> 49
<211> 22

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR and
 sequencing (beta4Gal-T7 exon 3)

 <400> 49
 gctctgagca gagcaggctg tc 22

 <210> 50
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 5' primer for PCR and
 sequencing (beta4Gal-T7 exon 4)

 <400> 50
 agatgggccc agtgacgctg ct 22

 <210> 51
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR and
 sequencing (beta4Gal-T7 exon 4)

 <400> 51
 ctcagggcag ccaccgcagc t 21

 <210> 52
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 5' primer for PCR and
 sequencing (beta4Gal-T7 exon 5)

 <400> 52
 aagggcagcc tgaccccgac tt 22

 <210> 53
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR and

sequencing (beta4Gal-T7 exon 5)

<400> 53
atgaccacct atccgtcccc aat 23

<210> 54
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and
sequencing (beta4Gal-T7 exon 6)

<400> 54
cagccctgag tccgtgctct tt 22

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and
sequencing (beta4Gal-T7 exon 6)

<400> 55
tggcctgtag gtacaggctt cct 23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for RT-PCR (K3)

<400> 56
cccagaaaaa gtccttcacg atg 23

<210> 57
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for RT-PCR (K3)

<400> 57
aactcttcta atttgtcacc tttgatgtag 30

<210> 58

<211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Probe for RT-PCR (K3)

 <400> 58
 atgagtgggtt catgcgc 17

 <210> 59
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 5' primer for RT-PCR (K11)

 <400> 59
 gctgaactgg aacgcacgta 20

 <210> 60
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for RT-PCR (K11)

 <400> 60
 cgggatgggtg ctggaatac 19

 <210> 61
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Probe for RT-PCR (K11)

 <400> 61
 agatccagga gttacagtgg 20

 <210> 62
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 5' primer for RT-PCR
 (beta4Gal-T7)

 <400> 62

cggcgcatta agggagct

18

<210> 63
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for RT-PCR
(beta4Gal-T7)

<400> 63
taccagttg tgattcccga g

21

<210> 64
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe for RT-PCR
(beta4Gal-T7)

<400> 64
ctccagcttt tccg

14

<210> 65
<211> 2652
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (1)..(2652)

<400> 65
atg gcc gtg cgc tcc cgc cgc cca tgg gtg agc gtg gca ttg ggg ttg
Met Ala Val Arg Ser Arg Arg Pro Trp Val Ser Val Ala Leu Gly Leu
1 5 10 15

48

gtc ctg ggc ttc acc gcc gcg tcc tgg ctc atc gcc ccc cgg gtg gcc
Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala
20 25 30

96

gag ctg agc gag aag agg cga cgc ggc tcc agt ctt tgc tcc tac tac
Glu Leu Ser Glu Lys Arg Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr
35 40 45

144

ggc cgc tcg gct acc ggg ccc cgc gcg gac gcg cag cag ctg ctc ccc
Gly Arg Ser Ala Thr Gly Pro Arg Ala Asp Ala Gln Gln Leu Leu Pro
50 55 60

192

caa ccc cag tcc cgg ccg cgg cta gag cag tcg ccg ccc cct gcc agc	240
Gln Pro Gln Ser Arg Pro Arg Leu Glu Gln Ser Pro Pro Pro Ala Ser	
65 70 75 80	
cac gag ctc ccc ggt cct cag cag ccg gag gcg gcg ccc gga ggt ccc	288
His Glu Leu Pro Gly Pro Gln Gln Pro Glu Ala Ala Pro Gly Gly Pro	
85 90 95	
agt ttt cgg agc agc ccc tgg cag cag ccg gct ctg ttg ccg cag agg	336
Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Ala Leu Leu Pro Gln Arg	
100 105 110	
agg cga gga cac acg ccc gaa ggt gcg acg gcg ctt ccc ggc gct ccg	384
Arg Arg Gly His Thr Pro Glu Gly Ala Thr Ala Leu Pro Gly Ala Pro	
115 120 125	
gct gcc aaa ggg gaa cca gag gag gag gat ggg ggc gcg gct gac cct	432
Ala Ala Lys Gly Glu Pro Glu Glu Glu Asp Gly Gly Ala Ala Asp Pro	
130 135 140	
cgg aag ggt ggc cgg ccg ggg agc agc cac aac ggc agc ggg gac ggg	480
Arg Lys Gly Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly	
145 150 155 160	
ggt gcc gct gtc ccg acc tcc gga ccc ggg gac ttc ctg tac gtg ggt	528
Gly Ala Ala Val Pro Thr Ser Gly Pro Gly Asp Phe Leu Tyr Val Gly	
165 170 175	
gtg atg acc gca cag aag tac ctg ggc agt cgc gcg ctg gcc gcg cag	576
Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln	
180 185 190	
cgg acc tgg gcg cgc ttc atc cct ggc cgc gtg gag ttc ttt tcc agt	624
Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser	
195 200 205	
cag caa tct ccc agt gct gcg ctt ggc cag ccc ccg cca cct ttg cct	672
Gln Gln Ser Pro Ser Ala Ala Leu Gly Gln Pro Pro Pro Pro Leu Pro	
210 215 220	
gtc atc gcg ctg cca ggg gtc gac gat tcc tac cct ccc cag aaa aag	720
Val Ile Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys	
225 230 235 240	
tcc ttc atg atg atc aag tac atg cac gac cac tat ctg gac aag tat	768
Ser Phe Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr	
245 250 255	
gag tgg ttc atg cgc gcc gac gac gat gtc tac atc aaa ggt gat aag	816
Glu Trp Phe Met Arg Ala Asp Asp Val Tyr Ile Lys Gly Asp Lys	
260 265 270	
tta gaa gaa ttt cta aga tcc cta aat agc agc aag cct ctc tac ctg	864
Leu Glu Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu	
275 280 285	

gga cag acg ggc ctg ggc aat act gaa gaa ctt gga aag ctg ggg ctg Gly Gln Thr Gly Leu Gly Asn Thr Glu Glu Leu Gly Lys Leu Gly Leu 290 295 300	912
gag ccc ggg gag aac ttc tgc atg gga gga cct ggc atg atc ttc agc Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser 305 310 315 320	960
aga gag gtt ctc agg cgg atg gtg cct cat atc ggc gaa tgc ctc cga Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg 325 330 335	1008
gag atg tac acc aca cac gaa gac gta gaa gta gga agg tgt gtt cgc Glu Met Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg 340 345 350	1056
cgt ttc ggc ggg acg cag tgt gtc tgg tct tat gag atg cag cag ctg Arg Phe Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu 355 360 365	1104
ttc cat gaa aac tac gaa cac aat cgc aag ggt tac atc caa gac ctc Phe His Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu 370 375 380	1152
cac aac agc aaa atc cac gca gcc atc acg ctc cat ccg aac aaa agg His Asn Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg 385 390 395 400	1200
ccc gcg tac cag tac aga ctt cat aac tac atg ctc agc cgc aag atc Pro Ala Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile 405 410 415	1248
tcc gag ctc cgc tac cgc acc atc cag ctc cac cgg gag agc gct ctc Ser Glu Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu 420 425 430	1296
atg agc aag ctc agc aac agt gaa gtg agc aaa gag gac caa cag ctg Met Ser Lys Leu Ser Asn Ser Glu Val Ser Lys Glu Asp Gln Gln Leu 435 440 445	1344
gga agg acg ccg tcc ttc aac cac ttc cag cct cgg gag aga aat gaa Gly Arg Thr Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu 450 455 460	1392
gtc atg gag tgg gag ttc ctg acg ggg aag ctg ctt tac tca gct gca Val Met Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala 465 470 475 480	1440
gag aac cag cct cct cga cag agc atc aac agc atc cta agg tca gct Glu Asn Gln Pro Pro Arg Gln Ser Ile Asn Ser Ile Leu Arg Ser Ala 485 490 495	1488
ctg gat gac act gtc ctg cag gtg atg gag atg atc aac gag aat gcc Leu Asp Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala 500 505 510	1536

aag agt agg ggc cga ctc atc gac ttc aag gaa att cag tat ggc tac	1584
Lys Ser Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr	
515 520 525	
cgc agg gtt gat ccc atg cac ggg gtt gag tac ata ttg gac ctg cta	1632
Arg Arg Val Asp Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu	
530 535 540	
ctc ctg tac aaa agg cac aaa gga agg aaa ctg act gtg cct gtg agg	1680
Leu Leu Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg	
545 550 555 560	
cgc cat gcc tat ctt cag cag cca ttt agc aag cct ttc ttc aga gag	1728
Arg His Ala Tyr Leu Gln Gln Pro Phe Ser Lys Pro Phe Phe Arg Glu	
565 570 575	
gtg gaa gaa ctc gac gtc aac cgt ctg gtg gag agt atc aac agc ggt	1776
Val Glu Glu Leu Asp Val Asn Arg Leu Val Glu Ser Ile Asn Ser Gly	
580 585 590	
aca cag tca ttc tcc gtt ata tcc aat tct cta aaa att ctc tct tct	1824
Thr Gln Ser Phe Ser Val Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser	
595 600 605	
ctt caa gag gcc aaa gac ata gga ggg cac aat gaa aag aaa gta cac	1872
Leu Gln Glu Ala Lys Asp Ile Gly Gly His Asn Glu Lys Lys Val His	
610 615 620	
att ctc gtt cca ctc gtt gga agg tac gac att ttc ttg aga ttc atg	1920
Ile Leu Val Pro Leu Val Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met	
625 630 635 640	
gaa aat ttt gaa agt acg tgt ctt atc cca aag caa aat gtc aag ctt	1968
Glu Asn Phe Glu Ser Thr Cys Leu Ile Pro Lys Gln Asn Val Lys Leu	
645 650 655	
gtc atc atc ctt ttc agc agg gat gct ggc caa gag tcc atc aag cac	2016
Val Ile Ile Leu Phe Ser Arg Asp Ala Gly Gln Glu Ser Ile Lys His	
660 665 670	
att gag ctg ata caa gaa tat cag agc agg tat ccc agt gca gaa atg	2064
Ile Glu Leu Ile Gln Glu Tyr Gln Ser Arg Tyr Pro Ser Ala Glu Met	
675 680 685	
atg ctc att ccc atg aag gga gag ttt tcc aga ggt ctt ggt ctt gaa	2112
Met Leu Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu	
690 695 700	
atg gct tct tcc cag ttt gac aat gac aca ttg ctg cta ttt tgt gat	2160
Met Ala Ser Ser Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp	
705 710 715 720	
gtt gac ttg att ttc aga gga gac ttc ctc caa cgc tgt cga gac aat	2208
Val Asp Leu Ile Phe Arg Gly Asp Phe Leu Gln Arg Cys Arg Asp Asn	
725 730 735	

aca gtt cag gga caa cag gta tat tac ccc atc atc ttt agc cag tat	2256
Thr Val Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr	
740 745 750	
gac cca aag gtc acc cat atg aga aat cct ccc aca gag ggt gac ttt	2304
Asp Pro Lys Val Thr His Met Arg Asn Pro Pro Thr Glu Gly Asp Phe	
755 760 765	
gta ttc tca aag gaa act ggg ttt tgg aga gac tat ggc tac gga atc	2352
Val Phe Ser Lys Glu Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile	
770 775 780	
aca tgc att tac aaa agc gat cta ctg ggt gca ggt gga ttt gat acc	2400
Thr Cys Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr	
785 790 795 800	
tca ata caa ggc tgg gga ctg gaa gat gta gat ctc tat aat aaa gtc	2448
Ser Ile Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val	
805 810 815	
atc cta tct ggc tta cgg ccc ttc aga agt caa gaa gtg gga gtg gtg	2496
Ile Leu Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val	
820 825 830	
cat att ttc cat cct gtt cat tgt gat cct aac ttg gac cct aag cag	2544
His Ile Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln	
835 840 845	
tat aag atg tgc tta gga tcc aaa gca agt act ttt gcc tca acc atg	2592
Tyr Lys Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met	
850 855 860	
caa ctg gct gaa ctc tgg tta gaa aaa cat ttg ggt gtc agg gat aat	2640
Gln Leu Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Asp Asn	
865 870 875 880	
cga act ctc tcc	2652
Arg Thr Leu Ser	

<210> 66
 <211> 884
 <212> PRT
 <213> mouse

<400> 66
 Met Ala Val Arg Ser Arg Arg Pro Trp Val Ser Val Ala Leu Gly Leu
 1 5 10 15
 Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala
 20 25 30
 Glu Leu Ser Glu Lys Arg Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr
 35 40 45
 Gly Arg Ser Ala Thr Gly Pro Arg Ala Asp Ala Gln Gln Leu Leu Pro
 50 55 60

Gln Pro Gln Ser Arg Pro Arg Leu Glu Gln Ser Pro Pro Pro Ala Ser
 65 70 75 80
 His Glu Leu Pro Gly Pro Gln Gln Pro Glu Ala Ala Pro Gly Gly Pro
 85 90 95
 Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Ala Leu Leu Pro Gln Arg
 100 105 110
 Arg Arg Gly His Thr Pro Glu Gly Ala Thr Ala Leu Pro Gly Ala Pro
 115 120 125
 Ala Ala Lys Gly Glu Pro Glu Glu Glu Asp Gly Gly Ala Ala Asp Pro
 130 135 140
 Arg Lys Gly Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly
 145 150 155 160
 Gly Ala Ala Val Pro Thr Ser Gly Pro Gly Asp Phe Leu Tyr Val Gly
 165 170 175
 Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln
 180 185 190
 Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser
 195 200 205
 Gln Gln Ser Pro Ser Ala Ala Leu Gly Gln Pro Pro Pro Pro Leu Pro
 210 215 220
 Val Ile Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys
 225 230 235 240
 Ser Phe Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr
 245 250 255
 Glu Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Lys
 260 265 270
 Leu Glu Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu
 275 280 285
 Gly Gln Thr Gly Leu Gly Asn Thr Glu Glu Leu Gly Lys Leu Gly Leu
 290 295 300
 Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser
 305 310 315 320
 Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg
 325 330 335
 Glu Met Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg
 340 345 350
 Arg Phe Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu
 355 360 365

Phe His Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu
370 375 380
His Asn Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg
385 390 395 400
Pro Ala Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile
405 410 415
Ser Glu Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu
420 425 430
Met Ser Lys Leu Ser Asn Ser Glu Val Ser Lys Glu Asp Gln Gln Leu
435 440 445
Gly Arg Thr Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu
450 455 460
Val Met Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala
465 470 475 480
Glu Asn Gln Pro Pro Arg Gln Ser Ile Asn Ser Ile Leu Arg Ser Ala
485 490 495
Leu Asp Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala
500 505 510
Lys Ser Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr
515 520 525
Arg Arg Val Asp Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu
530 535 540
Leu Leu Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg
545 550 555 560
Arg His Ala Tyr Leu Gln Gln Pro Phe Ser Lys Pro Phe Phe Arg Glu
565 570 575
Val Glu Glu Leu Asp Val Asn Arg Leu Val Glu Ser Ile Asn Ser Gly
580 585 590
Thr Gln Ser Phe Ser Val Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser
595 600 605
Leu Gln Glu Ala Lys Asp Ile Gly Gly His Asn Glu Lys Lys Val His
610 615 620
Ile Leu Val Pro Leu Val Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met
625 630 635 640
Glu Asn Phe Glu Ser Thr Cys Leu Ile Pro Lys Gln Asn Val Lys Leu
645 650 655
Val Ile Ile Leu Phe Ser Arg Asp Ala Gly Gln Glu Ser Ile Lys His
660 665 670

Ile Glu Leu Ile Gln Glu Tyr Gln Ser Arg Tyr Pro Ser Ala Glu Met
 675 680 685
 Met Leu Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu
 690 695 700
 Met Ala Ser Ser Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp
 705 710 715 720
 Val Asp Leu Ile Phe Arg Gly Asp Phe Leu Gln Arg Cys Arg Asp Asn
 725 730 735
 Thr Val Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr
 740 745 750
 Asp Pro Lys Val Thr His Met Arg Asn Pro Pro Thr Glu Gly Asp Phe
 755 760 765
 Val Phe Ser Lys Glu Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile
 770 775 780
 Thr Cys Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr
 785 790 795 800
 Ser Ile Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val
 805 810 815
 Ile Leu Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val
 820 825 830
 His Ile Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln
 835 840 845
 Tyr Lys Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met
 850 855 860
 Gln Leu Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Asp Asn
 865 870 875 880
 Arg Thr Leu Ser

<210> 67
 <211> 2490
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (1)..(2325)

<400> 67

atg cgg gcg tcg ctg ctg ctg tcc gtg ctg cgg ccc gcg ggg ccc gtg Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro Val 1 5 10 15	48
gcc gtg ggc atc tct ctg ggc ttc acc ctg agc ctg ctc agc gtc acc Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr 20 25 30	96
tgg gtg gag gag cct tgc gga ccc ggg ccg ccc caa ccc gga gac tct Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro Gly Asp Ser 35 40 45	144
gag ctg ccg ccg cgc ggc aac acc aac gcg gcg cgc cgg ccc aac tcg Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser 50 55 60	192
gtg cag ccc gga tcc gag cgc gag agg ccc ggg gcc ggc gca ggc acc Val Gln Pro Gly Ser Glu Arg Glu Arg Pro Gly Ala Gly Ala Gly Thr 65 70 75 80	240
ggc gag agc tgg gag cct cgt gtc ttg ccc tac cat ccc gcg cag cca Gly Glu Ser Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro 85 90 95	288
ggc cag gcc acc aag aag gcc gtc aga act cgg tat atc agc acg gag Gly Gln Ala Thr Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu 100 105 110	336
ctg ggc atc agg cag aag ctt ctg gtg gca gtg ctg acc tca caa gcc Leu Gly Ile Arg Gln Lys Leu Leu Val Ala Val Leu Thr Ser Gln Ala 115 120 125	384
acg ttg cct aca ctg ggt gtg gct gta aac cga act ctg gga cac cga Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg 130 135 140	432
ctg gag cat gta gtg ttc ctg acc ggt gcg agg ggc cgc cgg aca cct Leu Glu His Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Thr Pro 145 150 155 160	480
tca ggc atg gcg gtg gtg gca ctg ggc gaa gag agg ccc atc gga cac Ser Gly Met Ala Val Val Ala Leu Gly Glu Glu Arg Pro Ile Gly His 165 170 175	528
ctg cac ctg gcg ctg cgc cac ctg ctg gag caa cac ggc gat gac ttt Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe 180 185 190	576
gac tgg ttt ttc cta gtg cct gat gcc acc tat act gaa gcg cat gga Asp Trp Phe Phe Leu Val Pro Asp Ala Thr Tyr Thr Glu Ala His Gly 195 200 205	624
ctg gac cgc cta gct ggc cac ctc agc ctt gct tca gca acc cat ctc Leu Asp Arg Leu Ala Gly His Leu Ser Leu Ala Ser Ala Thr His Leu 210 215 220	672

tat ctt ggc cgg ccg cag gac ttc atc ggt gga gat act acc cca ggc	720
Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Asp Thr Thr Pro Gly	
225 230 235 240	
cgc tac tgc cac ggg ggc ttt gga gtc ttg ctc tct cgc aca ctg cta	768
Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Thr Leu Leu	
245 250 255	
cag caa ctg cgc ccc cac ctg gaa agc tgc cgc aac gac atc gtc agt	816
Gln Gln Leu Arg Pro His Leu Glu Ser Cys Arg Asn Asp Ile Val Ser	
260 265 270	
gct cgc ccg gat gag tgg ttg ggc cgc tgc atc ctt gat gcc aca ggc	864
Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly	
275 280 285	
gtg ggc tgt act ggt gac cac gag gga atg cac tac aac tac ctg gaa	912
Val Gly Cys Thr Gly Asp His Glu Gly Met His Tyr Asn Tyr Leu Glu	
290 295 300	
ctg agc ccc ggg gag cct gta cag gag ggg gac cct cgt ttc cgc agc	960
Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro Arg Phe Arg Ser	
305 310 315 320	
gcc ttg aca gcc cat ccc gtg cgt gac cct gtg cac atg tac cag ctg	1008
Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu	
325 330 335	
cac aaa gct ttt gcc cgc gct gag ctg gac cgc acg tac cag gag att	1056
His Lys Ala Phe Ala Arg Ala Glu Leu Asp Arg Thr Tyr Gln Glu Ile	
340 345 350	
caa gaa ttg cag tgg gag atc cag aat acc agc cga ctg gct gct gat	1104
Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser Arg Leu Ala Ala Asp	
355 360 365	
ggg gag aga gcc tct gcc tgg cca gtg ggc atc cca gca ccg tct cgc	1152
Gly Glu Arg Ala Ser Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg	
370 375 380	
cct gcc tca cgc ttt gag gtt ctg cgc tgg gac tac ttc aca gaa caa	1200
Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln	
385 390 395 400	
tac gcg ttc tcc tgc gcc gat ggc tct ccc cgc tgc ccg ttg cgt ggg	1248
Tyr Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly	
405 410 415	
gcc gac cag gct gat gtg gct gac gtc ctg ggg aca gcc tta gag gag	1296
Ala Asp Gln Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu	
420 425 430	
ctc aac cgc cgt tac cag cca gcg ctg cag ctc cag aag caa cag ctg	1344
Leu Asn Arg Arg Tyr Gln Pro Ala Leu Gln Leu Gln Lys Gln Gln Leu	
435 440 445	

gtg aac ggc tac cgg cgt ttt gat cca gcc cga ggc atg gag tac aca Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr 450 455 460	1392
cta gac ctg cag ctg gaa gcg ctg aca ccc cag ggt ggc cgc tgg ccc Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Trp Pro 465 470 475 480	1440
ctc acc cgc agg gtg cag ctc ctt cgg ccc ttg agc cga gtg gag atc Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile 485 490 495	1488
ttg cct gta ccc tat gtc acc gag gct tct cgg ctc act gtg cta ctg Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu 500 505 510	1536
ccg ctg gct gca gcg gaa cga gac ctg gct tct ggc ttc tta gaa gcc Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Ser Gly Phe Leu Glu Ala 515 520 525	1584
ttt gcc act gca gcc ctg gaa cct ggt gat gca gca gcc ttg acc ctg Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Leu Thr Leu 530 535 540	1632
ctg ctg ctg tat gag cca cgc cag gcc cag cgg gca gcc cac tca gac Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Ala Ala His Ser Asp 545 550 555 560	1680
gtc ttc gca cct gtc aag gcc cac gtg gca gag cta gag cgg cgt ttc Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg Phe 565 570 575	1728
cct ggt gcc cgg gtg ccc tgg ctc agt gtg cag aca gca gcg ccc tct Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro Ser 580 585 590	1776
cca ctg cgt ctc atg gat ctg ctg tcc aag aag cac cca cta gac act Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp Thr 595 600 605	1824
ctg ttc ctg ctg gcc ggg cca gac acg gta ctc aca cct gat ttc ctg Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe Leu 610 615 620	1872
aac cgc tgc cgc atg cat gcc atc tct ggc tgg cag gcc ttc ttc ccc Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro 625 630 635 640	1920
atg cac ttc cag gcc ttc cac cct gct gtg gct cct cct cag ggc cct Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly Pro 645 650 655	1968
ggg cca cca gag ctg ggc cgt gac acc ggt cac ttt gat cgc cag gct Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly His Phe Asp Arg Gln Ala 660 665 670	2016

gcc agt gag gca tgc ttc tac aac tcc gac tat gtg gcg gcc cgt ggc 2064
 Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly
 675 680 685
 cgg ctg gtg gcg gcc tcg gag cag gag gag gag ctg ctg gag agc ctg 2112
 Arg Leu Val Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser Leu
 690 695 700
 gat gtg tac gag ttg ttt ctg cgc ttc tcc aac ttg cac gtg ctg aga 2160
 Asp Val Tyr Glu Leu Phe Leu Arg Phe Ser Asn Leu His Val Leu Arg
 705 710 715 720
 gca gta gag cca gcc ttg ctg cag cgc tac cgg gcc cag ccg tgc agt 2208
 Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Pro Cys Ser
 725 730 735
 gca cgg ctc agt gaa gac ctt tac cac cgc tgt cgc cag agc gta ctt 2256
 Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Arg Gln Ser Val Leu
 740 745 750
 gag ggc ctt ggc tcc cgc acc cag ctt gcc atg ctg ctc ttt gag cag 2304
 Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu Gln
 755 760 765
 gaa cag ggg aac agc acc taa gccctgcac ctgtccctgc tcttccccag 2355
 Glu Gln Gly Asn Ser Thr
 770
 gaacctggag ccacgtgcc aacctcgtgg acagggctgg ctgtagcctc agtccttagg 2415
 gcagcccact ggtcccttgt ctcttgcttt gttggacca tgggctcagg acaagccctg 2475
 agacagatgc cctag 2490

<210> 68
 <211> 774
 <212> PRT
 <213> mouse

<400> 68
 Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro Val
 1 5 10 15
 Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr
 20 25 30
 Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro Gly Asp Ser
 35 40 45
 Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser
 50 55 60
 Val Gln Pro Gly Ser Glu Arg Glu Arg Pro Gly Ala Gly Ala Gly Thr
 65 70 75 80

Gly Glu Ser Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro
 85 90 95
 Gly Gln Ala Thr Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu
 100 105 110
 Leu Gly Ile Arg Gln Lys Leu Leu Val Ala Val Leu Thr Ser Gln Ala
 115 120 125
 Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg
 130 135 140
 Leu Glu His Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Thr Pro
 145 150 155 160
 Ser Gly Met Ala Val Val Ala Leu Gly Glu Glu Arg Pro Ile Gly His
 165 170 175
 Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe
 180 185 190
 Asp Trp Phe Phe Leu Val Pro Asp Ala Thr Tyr Thr Glu Ala His Gly
 195 200 205
 Leu Asp Arg Leu Ala Gly His Leu Ser Leu Ala Ser Ala Thr His Leu
 210 215 220
 Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Asp Thr Thr Pro Gly
 225 230 235 240
 Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Thr Leu Leu
 245 250 255
 Gln Gln Leu Arg Pro His Leu Glu Ser Cys Arg Asn Asp Ile Val Ser
 260 265 270
 Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly
 275 280 285
 Val Gly Cys Thr Gly Asp His Glu Gly Met His Tyr Asn Tyr Leu Glu
 290 295 300
 Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro Arg Phe Arg Ser
 305 310 315 320
 Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu
 325 330 335
 His Lys Ala Phe Ala Arg Ala Glu Leu Asp Arg Thr Tyr Gln Glu Ile
 340 345 350
 Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser Arg Leu Ala Ala Asp
 355 360 365
 Gly Glu Arg Ala Ser Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg
 370 375 380

Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln
 385 390 395 400
 Tyr Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly
 405 410 415
 Ala Asp Gln Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu
 420 425 430
 Leu Asn Arg Arg Tyr Gln Pro Ala Leu Gln Leu Gln Lys Gln Gln Leu
 435 440 445
 Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr
 450 455 460
 Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Trp Pro
 465 470 475 480
 Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile
 485 490 495
 Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu
 500 505 510
 Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Ser Gly Phe Leu Glu Ala
 515 520 525
 Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Leu Thr Leu
 530 535 540
 Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Ala Ala His Ser Asp
 545 550 555 560
 Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg Phe
 565 570 575
 Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro Ser
 580 585 590
 Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp Thr
 595 600 605
 Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe Leu
 610 615 620
 Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro
 625 630 635 640
 Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly Pro
 645 650 655
 Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly His Phe Asp Arg Gln Ala
 660 665 670
 Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly
 675 680 685

Arg Leu Val Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser Leu
 690 695 700
 Asp Val Tyr Glu Leu Phe Leu Arg Phe Ser Asn Leu His Val Leu Arg
 705 710 715 720
 Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Pro Cys Ser
 725 730 735
 Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Arg Gln Ser Val Leu
 740 745 750
 Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu Gln
 755 760 765
 Glu Gln Gly Asn Ser Thr
 770

<210> 69
 <211> 984
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (1)..(984)

<400> 69
 atg ttg ccc tcc cgg agg aaa gcg gcg cag ctg ccc tgg gag gat ggc 48
 Met Leu Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly
 1 5 10 15
 agg gcc agg ttg ctt cct gga ggc ctc cgc cgg aaa tgc tcc atc ttc 96
 Arg Ala Arg Leu Leu Pro Gly Gly Leu Arg Arg Lys Cys Ser Ile Phe
 20 25 30
 cac ctc ttc att gcc ttt ctc ctg ttg gtc ttc ttc tcc ctg ctc tgg 144
 His Leu Phe Ile Ala Phe Leu Leu Leu Val Phe Phe Ser Leu Leu Trp
 35 40 45
 ctg cag ctc agc tgt tct gga gat atg gcc cag gtg acc agg gga caa 192
 Leu Gln Leu Ser Cys Ser Gly Asp Met Ala Gln Val Thr Arg Gly Gln
 50 55 60
 ggg caa gag acc tcg ggt cca ccc cgg gct tgc cct cca gag ccg ccc 240
 Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
 65 70 75 80
 cct gag cac tgg gaa gaa gat gag tcc tgg ggg ccc cac cgc ttg gca 288
 Pro Glu His Trp Glu Glu Asp Glu Ser Trp Gly Pro His Arg Leu Ala
 85 90 95
 gtg ctg gtg ccc ttt cgt gag cgc ttt gag gag ctg ctg gtc ttt gtg 336
 Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
 100 105 110

ccc cac atg cac cgc ttc cta agc agg aag agg atc cag cac cac atc	384
Pro His Met His Arg Phe Leu Ser Arg Lys Arg Ile Gln His His Ile	
115 120 125	
tat gtg ctc aac cag gtg gac cat ttc agg ttc aat cgg gca gca ctc	432
Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu	
130 135 140	
atc aat gtg ggc ttc ctg gag agc agc aac agc aca gac tac atc gcc	480
Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala	
145 150 155 160	
atg cac gat gtg gac ctg ctc cct ctc aat gag gag ctg gac tat ggc	528
Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly	
165 170 175	
ttc ccg gag gct ggg ccc ttc cat gtg gcc tcc cca gag ctc cac cct	576
Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro	
180 185 190	
ctc tac cac tac aag acc tat gtg ggc ggc att ctg ctg ctg tcc aaa	624
Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys	
195 200 205	
cag cac tac cag ctg tgc aac gga atg tcc aac cgc ttt tgg ggc tgg	672
Gln His Tyr Gln Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp	
210 215 220	
ggc cga gag gat gat gaa ttc tac cgg cgc atc aaa gga gct ggc ctc	720
Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu	
225 230 235 240	
cag ctt ttc cgc ccc tgc gga atc aca act ggg tac cag aca ttt cgc	768
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Gln Thr Phe Arg	
245 250 255	
cac ttg cat gac cct gcc tgg cgg aag agg gac caa aaa cgc att gcg	816
His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala	
260 265 270	
gct caa aaa cag gaa cag ttc aag gtg gac cgg gag gga ggc ctg aac	864
Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn	
275 280 285	
act gtg aag tac cgg gtg gat tcc cgc acg gca ctg tct ata gga ggg	912
Thr Val Lys Tyr Arg Val Asp Ser Arg Thr Ala Leu Ser Ile Gly Gly	
290 295 300	
gcc ccg tgc act gtc ctc aat gtc atg ctg gac tgc gat aaa aca gcc	960
Ala Pro Cys Thr Val Leu Asn Val Met Leu Asp Cys Asp Lys Thr Ala	
305 310 315 320	
acc cca tgg tgc ata ttt ggc tga	984
Thr Pro Trp Cys Ile Phe Gly	
325	

<210> 70
 <211> 327
 <212> PRT
 <213> mouse

<400> 70

Met	Leu	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp	Gly
1			5						10					15	
Arg	Ala	Arg	Leu	Leu	Pro	Gly	Gly	Leu	Arg	Arg	Lys	Cys	Ser	Ile	Phe
			20					25					30		
His	Leu	Phe	Ile	Ala	Phe	Leu	Leu	Leu	Val	Phe	Phe	Ser	Leu	Leu	Trp
		35					40					45			
Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Met	Ala	Gln	Val	Thr	Arg	Gly	Gln
	50					55					60				
Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys	Pro	Pro	Glu	Pro	Pro
65					70					75					80
Pro	Glu	His	Trp	Glu	Glu	Asp	Glu	Ser	Trp	Gly	Pro	His	Arg	Leu	Ala
				85					90					95	
Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe	Glu	Glu	Leu	Leu	Val	Phe	Val
			100					105					110		
Pro	His	Met	His	Arg	Phe	Leu	Ser	Arg	Lys	Arg	Ile	Gln	His	His	Ile
		115					120					125			
Tyr	Val	Leu	Asn	Gln	Val	Asp	His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu
	130					135					140				
Ile	Asn	Val	Gly	Phe	Leu	Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala
145					150					155					160
Met	His	Asp	Val	Asp	Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly
				165					170					175	
Phe	Pro	Glu	Ala	Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro
			180					185					190		
Leu	Tyr	His	Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys
		195					200					205			
Gln	His	Tyr	Gln	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp
	210					215					220				
Gly	Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu
225					230					235					240
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Gln	Thr	Phe	Arg
				245					250					255	
His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg	Ile	Ala
			260					265					270		

Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
275 280 285

Thr Val Lys Tyr Arg Val Asp Ser Arg Thr Ala Leu Ser Ile Gly Gly
290 295 300

Ala Pro Cys Thr Val Leu Asn Val Met Leu Asp Cys Asp Lys Thr Ala
305 310 315 320

Thr Pro Trp Cys Ile Phe Gly
325